

0590  
0429

#6



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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/995,898A

DATE: 05/02/2002  
 TIME: 17:22:38

Input Set : A:\00-108.txt  
 Output Set: N:\CRF3\05022002\I995898A.raw

4 <110> APPLICANT: Presnell, Scott R.  
 5 Xu, Wenfeng  
 6 Novak, Julia E.  
 7 Whitmore, Theodore E.  
 8 Grant, Francis J.  
 10 <120> TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19  
 13 <130> FILE REFERENCE: 00-108  
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/995,898A  
 C--> 15 <141> CURRENT FILING DATE: 2001-11-28  
 15 <150> PRIOR APPLICATION NUMBER: US 60/253,561  
 16 <151> PRIOR FILING DATE: 2000-11-28  
 18 <150> PRIOR APPLICATION NUMBER: US 60/267,211  
 19 <151> PRIOR FILING DATE: 2001-02-07  
 21 <160> NUMBER OF SEQ ID NOS: 50  
 23 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 1476  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Homo sapiens  
 30 <220> FEATURE:  
 31 <221> NAME/KEY: CDS  
 32 <222> LOCATION: (1)...(1473)  
 34 <400> SEQUENCE: 1  
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 36 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln  
 37 1 5 10 15  
 39 gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg 96  
 40 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu  
 41 20 25 30  
 43 ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc 144  
 44 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly  
 45 35 40 45  
 47 aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc 192  
 48 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr  
 49 50 55 60  
 51 cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg 240  
 52 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu  
 53 65 70 75 80  
 55 cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc 288  
 56 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe  
 57 85 90 95  
 59 aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg 336  
 60 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val

ENTERED

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61		100		105		110		
63	gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca cct							384
64	Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro							
65		115		120		125		
67	gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc acg							432
68	Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr							
69		130		135		140		
71	tac cag ctg ccc ccc tgc atg ccc cca ctg ttt ctg aag tat gag gtg							480
72	Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Phe Leu Lys Tyr Glu Val							
73	145		150		155		160	
75	gca ttt tgg ggg ggg ggg gcc gga acc aag acc cta ttt cca gtc act							528
76	Ala Phe Trp Gly Gly Gly Ala Gly Thr Lys Thr Leu Phe Pro Val Thr							
77		165		170		175		
79	ccc cat ggc cag cca gtc cag atc act ctc cag cca gct gcc agc gaa							576
80	Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu							
81		180		185		190		
83	cac cac tgc ctc agt gcc aga acc atc tac acg ttc agt gtc ccg aaa							624
84	His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys							
85		195		200		205		
87	tac agc aag ttc tct aag ccc acc tgc ttc ttg ctg gag gtc cca gaa							672
88	Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu							
89		210		215		220		
91	gcc aac tgg gct ttc ctg gtg ctg cca tcg ctt ctg ata ctg ctg tta							720
92	Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu							
93	225		230		235		240	
95	gta att gcc gca ggg ggt gtg atc tgg aag acc ctc atg ggg aac ccc							768
96	Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro							
97		245		250		255		
99	tgg ttt cag cgg gca aag atg cca cgg gcc ctg gaa ctg acc aga ggg							816
100	Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Glu Leu Thr Arg Gly							
101		260		265		270		
103	gtc agg ccg acg cct cga gtc agg gcc cca gcc acc caa cag aca aga							864
104	Val Arg Pro Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg							
105		275		280		285		
107	tgg aag aag gac ctt gca gag gac gaa gag gag gag gat gag gag gac							912
108	Trp Lys Lys Asp Leu Ala Glu Asp Glu Glu Glu Glu Asp Glu Glu Asp							
109		290		295		300		
111	aca gaa gat ggc gtc agc ttc cag ccc tac att gaa cca cct tct ttc							960
112	Thr Glu Asp Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe							
113	305		310		315		320	
115	ctg ggg caa gag cac cag gct cca ggg cac tcg gag gct ggt ggg gtg							1008
116	Leu Gly Gln Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val							
117		325		330		335		
119	gac tca ggg agg ccc agg gct cct ctg gtc cca agc gaa ggc tcc tct							1056
120	Asp Ser Gly Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser							
121		340		345		350		
123	gct tgg gat tct tca gac aga agc tgg gcc agc act gtg gac tcc tcc							1104
124	Ala Trp Asp Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser							
125		355		360		365		

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127  tgg gac agg gct ggg tcc tct ggc tat ttg gct gag aag ggg cca ggc      1152
128  Trp Asp Arg Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly
129      370                      375                      380
131  caa ggg ccg ggt ggg gat ggg cac caa gaa tct ctc cca cca cct gaa      1200
132  Gln Gly Pro Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu
133      385                      390                      395                      400
135  ttc tcc aag gac tcg ggt ttc ctg gaa gag ctc cca gaa gat aac ctc      1248
136  Phe Ser Lys Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu
137      405                      410                      415
139  tcc tcc tgg gcc acc tgg ggc acc tta cca ccg gag ccg aat ctg gtc      1296
140  Ser Ser Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val
141      420                      425                      430
143  cct ggg gga ccc cca gtt tct ctt cag aca ctg acc ttc tgc tgg gaa      1344
144  Pro Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu
145      435                      440                      445
147  agc agc cct gag gag gaa gag gag gcg agg gaa tca gaa att gag gac      1392
148  Ser Ser Pro Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp
149      450                      455                      460
151  agc gat gcg ggc agc tgg ggg gct gag agc acc cag agg acc gag gac      1440
152  Ser Asp Ala Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp
153      465                      470                      475                      480
155  agg ggc cgg aca ttg ggg cat tac atg gcc agg tga      1476
156  Arg Gly Arg Thr Leu Gly His Tyr Met Ala Arg
157      485                      490
160 <210> SEQ ID NO: 2
161 <211> LENGTH: 491
162 <212> TYPE: PRT
163 <213> ORGANISM: Homo sapiens
165 <400> SEQUENCE: 2
166  Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Cys Leu Leu Gln
167      1      5      10      15
168  Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
169      20      25      30
170  Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
171      35      40      45
173  Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
174      50      55      60
175  Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
176      65      70      75      80
177  Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
178      85      90      95
179  Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
180      100     105     110
181  Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
182      115     120     125
183  Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
184      130     135     140
185  Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Phe Leu Lys Tyr Glu Val
186      145     150     155     160

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```

187  Ala Phe Trp Gly Gly Gly Ala Gly Thr Lys Thr Leu Phe Pro Val Thr
188                                165                                170                                175
189  Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu
190                                180                                185                                190
191  His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys
192                                195                                200                                205
193  Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu
194                                210                                215                                220
195  Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu
196  225                                230                                235                                240
197  Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro
198                                245                                250                                255
199  Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Glu Leu Thr Arg Gly
200                                260                                265                                270
201  Val Arg Pro Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg
202                                275                                280                                285
203  Trp Lys Lys Asp Leu Ala Glu Asp Glu Glu Glu Glu Asp Glu Glu Asp
204                                290                                295                                300
205  Thr Glu Asp Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe
206  305                                310                                315                                320
207  Leu Gly Gln Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val
208                                325                                330                                335
209  Asp Ser Gly Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser
210                                340                                345                                350
211  Ala Trp Asp Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser
212                                355                                360                                365
213  Trp Asp Arg Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly
214                                370                                375                                380
216  Gln Gly Pro Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu
217  385                                390                                395                                400
218  Phe Ser Lys Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu
219                                405                                410                                415
220  Ser Ser Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val
221                                420                                425                                430
222  Pro Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu
223                                435                                440                                445
224  Ser Ser Pro Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp
225                                450                                455                                460
226  Ser Asp Ala Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp
227  465                                470                                475                                480
228  Arg Gly Arg Thr Leu Gly His Tyr Met Ala Arg
229                                485                                490

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231 &lt;210&gt; SEQ ID NO: 3

232 &lt;211&gt; LENGTH: 1473

233 &lt;212&gt; TYPE: DNA

234 &lt;213&gt; ORGANISM: Artificial Sequence

236 &lt;220&gt; FEATURE:

237 &lt;223&gt; OTHER INFORMATION: Degenerate polynucleotide seuquence of SEQ ID NO:2

W--&gt; 239 &lt;221&gt; NAME/KEY: misc\_feature

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DATE: 05/02/2002

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TIME: 17:22:38

Input Set : A:\00-108.txt

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240 <222> LOCATION: (1)...(1473)
241 <223> OTHER INFORMATION: n = A,T,C or G
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W--> 244 atggcnggnc cngarmgntg gggncenytn ytnytnygyy tnytnccargc ngcncngggn      60
W--> 245 mgncncmgny tngcncncnc ncaraaygtg acnytnytnw snccaraaytt ywsngntntay      120
W--> 246 ytnacntggy tncnggnytn nggnaayccn caryaygtgna cntayttygt ngcntaycar      180
W--> 247 wsnwsnccna cnmgnmgngm ntggmgngar gtngargart gygcnggnac naargarytn      240
W--> 248 ytnygywsna tgatgtgyyt naaraarcar gayytnntaya ayaarttyaa rggnmngntn      300
W--> 249 mgnacngtnw snccnwsnws naarwsnccn tgggtngarw sngartayyt ngaytayytn      360
W--> 250 ttygargtng arcncngcnc nccngtnytn gtnytnacnc aracngarga rathytnwsn      420
W--> 251 gcnaaygcna cntaycaryt nccncntgy atgcncncny tnttyytnaa rtaygargtn      480
W--> 252 gcnttytggy gngngngngc nggnacnaar acnytnnttyc cngtnacncc ncayggncar      540
W--> 253 ccngtnccara thacnytnca rccngcngcn wsnrgarcayc aytgyytnws ngcnmgngn      600
W--> 254 athtayacnt tywsngtncc naartaywsn aarttywsna arccnacntg ytttyytnytn      660
W--> 255 gargtnccng argcnaaytg ggcnttyytn gtnytnccnw snytnytnat hytnytnytn      720
W--> 256 gtnathgcng cngngngngt nathtggaar acnytnatgg gnaayccntg gttycarmgn      780
W--> 257 gcnaaratgc cnmngngcny ngarytnacn mgngngngtnm gncncncc nmgngtnmgn      840
W--> 258 gcncngcna cncarcac nmgntggaar aargayytn cngargayga rgargargar      900
W--> 259 gaygargarg ayacngarga yggngtnwsn ttycarcent ayathgarcc nccnwsntty      960
W--> 260 ytngngcarg arcaycargc nccngngcay wsnrgargcng gngngngtna ywsngngmgn      1020
W--> 261 ccnmngcnc cnytnngtncc nwsngarggn wsnwsngcnt gggaywsnws ngaymgngnwsn      1080
W--> 262 tgggcnwsna cngtnaygws nwsntgggag mgngcnggnw snwsnggnta yytnngcngar      1140
W--> 263 aargngcng gncarggnc ngngngngay ggcaycarg arwsnytncc nccncngar      1200
W--> 264 ttywsnaarg aywsnggntt yytnngargar ytnccngarg ayaayytnws nwsntgggcn      1260
W--> 265 acntggggn cnytnccncc ngarccnaay ytnngtnccng gngngcncnc ngtnwsnytn      1320
W--> 266 caracnytna cnttytgtyg ggarwsnwsn ccngargarg argargargc nmngngarwsn      1380
W--> 267 garathgarg aywsngaygc nggnwsntgg gngcngarw snacncarmg nacngargay      1440
W--> 268 mgngngmgn cnytnngnca ytayatggcn mgn      1473
270 <210> SEQ ID NO: 4
271 <211> LENGTH: 203
272 <212> TYPE: PRT
273 <213> ORGANISM: Homo sapiens
275 <400> SEQUENCE: 4
276 Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu Leu Ser Gln Asn
277 1 5 10 15
278 Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly Asn Pro Gln Asp
279 20 25 30
280 Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr Arg Arg Arg Trp
281 35 40 45
282 Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu Leu Cys Ser Met
283 50 55 60
284 Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe Lys Gly Arg Val
285 65 70 75 80
286 Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val Glu Ser Glu Tyr
287 85 90 95
288 Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro Val Leu Val Leu
289 100 105 110
290 Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr Tyr Gln Leu Pro
291 115 120 125

```

RAW SEQUENCE LISTING ERROR SUMMARY  
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Input Set : A:\00-108.txt

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 6,9,12,18,24,27,30,33,36,42,45,51,54,57,60,63,66,69,72,75,78  
Seq#:3; N Pos. 81,90,93,96,99,102,114,117,123,126,132,135,138,141,144,150  
Seq#:3; N Pos. 159,162,171,174,183,186,189,192,195,198,201,207,213,225,228  
Seq#:3; N Pos. 231,240,243,249,261,276,294,297,300,303,306,309,312,315,318  
Seq#:3; N Pos. 321,327,330,336,342,351,360,369,375,378,381,384,387,390,393  
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Seq#:3; N Pos. 699,702,705,708,714,717,720,723,729,732,735,738,741,753,756  
Seq#:3; N Pos. 762,768,780,783,792,795,798,801,807,810,813,816,819,822,825  
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RAW SEQUENCE LISTING ERROR SUMMARY  
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Seq#:29; N Pos. 150,159,162,171,174,183,186,189,192,195,198,201,207,213,225  
Seq#:29; N Pos. 228,231,240,243,249,261,276,294,297,300,303,306,309,312,315  
Seq#:29; N Pos. 318,321,327,330,336,342,351,360,369,375,378,381,384,387,390  
Seq#:29; N Pos. 393,396,399,405,417,420,423,429,432,441,444,447,456,459,462  
Seq#:29; N Pos. 468,480,483,498,501,504,513,516,519,522,528,531,534,537,540  
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Seq#:29; N Pos. 603,606,609,618,624,627,633  
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